

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/051,843A

DATE: 03/01/2001
TIME: 12:24:37

Input Set : A:\sequence.asc
Output Set: N:\CRF3\03012001\I051843A.raw

4 <110> APPLICANT: Willson, Tracy
5 Nicola, Nicos A.
6 Hilton, Douglas J.
7 Metcalf, Donald
8 Zhang, Jian G.
10 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
11 ENCODING SAME
13 <130> FILE REFERENCE: Davies cc
15 <140> CURRENT APPLICATION NUMBER: 09/051,843A
16 <141> CURRENT FILING DATE: 1998-06-29
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1383
24 <212> TYPE: DNA
25 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (61)..(1338)
31 <220> FEATURE: /
32 <221> NAME/KEY: unsure
33 <222> LOCATION: (121)
34 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
35 region
37 <220> FEATURE: /
38 <221> NAME/KEY: unsure
39 <222> LOCATION: (122)
40 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
41 region
43 <220> FEATURE: /
44 <221> NAME/KEY: unsure
45 <222> LOCATION: (123)
46 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
47 region
49 <220> FEATURE: /
50 <221> NAME/KEY: unsure
51 <222> LOCATION: (640)
52 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
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55 <220> FEATURE: /
56 <221> NAME/KEY: unsure
57 <222> LOCATION: (641)
58 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
59 region
61 <220> FEATURE: /
62 <221> NAME/KEY: unsure
63 <222> LOCATION: (642)

ENTERED

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64 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
65 region
67 <400> SEQUENCE: 1
68 tgaaaagata gaataaatgg cctcgtgccg aattcggcac gagccgaggc gagggcctgc 60
71 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108
72 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
73 1 5 10 15
75 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
76 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Thr Glu Val Gln Pro
77 20 25 30
79 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
80 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
81 35 40 45
83 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
84 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
85 50 55 60
87 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
88 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
89 65 70 75 80
91 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
92 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
93 85 90 95
95 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
96 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
97 100 105 110
99 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
100 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
101 115 120 125
103 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
104 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
105 130 135 140
107 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
108 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
109 145 150 155 160
111 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
112 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
113 165 170 175
115 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
116 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
117 180 185 190
119 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat 684
120 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
121 195 200 205
123 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat 732
124 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
125 210 215 220
127 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt 780
128 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
129 225 230 235 240

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131 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc 828
132 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
133          245          250          255
135 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat 876
136 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
137          260          265          270
139 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga 924
140 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
141          275          280          285
143 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac 972
144 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
145          290          295          300
147 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt 1020
148 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
149 305          310          315          320
151 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt 1068
152 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
153          325          330          335
155 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca 1116
156 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
157          340          345          350
159 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg 1164
160 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
161          355          360          365
163 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt 1212
164 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
165          370          375          380
167 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag 1260
168 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
169 385          390          395          400
171 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg 1308
172 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
173          405          410          415
175 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc 1358
176 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
177          420          425
179 tttcttgccct tcaatgtgac cctgt 1383
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 426
185 <212> TYPE: PRT
186 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
188 <220> FEATURE:
189 <221> NAME/KEY: unsure
190 <222> LOCATION: (21)
191 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
193 <220> FEATURE:
194 <221> NAME/KEY: unsure
195 <222> LOCATION: (194)
196 <223> OTHER INFORMATION: authors are unsure about the sequence assignment

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MAR 08 2001

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Output Set: N:\CRF3\03012001\I051843A.raw

198 <400> SEQUENCE: 2

199 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
 200 1 5 10 15
 202 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
 203 20 25 30
 205 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
 206 35 40 45
 208 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
 209 50 55 60
 211 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 212 65 70 75 80
 214 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
 215 85 90 95
 217 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
 218 100 105 110
 220 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 221 115 120 125
 223 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 224 130 135 140
 226 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
 227 145 150 155 160
 229 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
 230 165 170 175
 232 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
 233 180 185 190
 235 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
 236 195 200 205
 238 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
 239 210 215 220
 241 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Lys Asn Gly
 242 225 230 235 240
 244 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
 245 245 250 255
 247 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
 248 260 265 270
 250 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
 251 275 280 285
 253 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
 254 290 295 300
 256 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
 257 305 310 315 320
 259 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
 260 325 330 335
 262 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
 263 340 345 350
 265 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
 266 355 360 365
 268 Leu Lys Ile Ile Ile Phe Pro Ile Pro Asp Pro Gly Lys Ile Phe
 269 370 375 380

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271 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
272 385                      390                      395                      400
274 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
275                      405                      410                      415
277 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
278                      420                      425
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282 <211> LENGTH: 1383
283 <212> TYPE: DNA
284 <213> ORGANISM: Human IL-13 receptor alpha-chain
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (61)..(1338)
290 <400> SEQUENCE: 3
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294 atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc 108
295 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
296 1                      5                      10                      15
298 gcc ggc ggc ggg ggc ggg ggc ggc ggc ggc cct acg gaa act cag cca 156
299 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
300                      20                      25                      30
302 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
303 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
304                      35                      40                      45
306 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
307 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
308 50                      55                      60
310 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
311 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
312 65                      70                      75                      80
314 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
315 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
316                      85                      90                      95
318 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
319 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
320                      100                      105                      110
322 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
323 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
324                      115                      120                      125
326 act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct 492
327 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
328 130                      135                      140
330 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac 540
331 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
332 145                      150                      155                      160
334 tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt 588
335 Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
336                      165                      170                      175
338 aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag 636

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PMI

Please Note:

Use of n and/ r Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 03/01/2001
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Input Set : A:\sequence.asc
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L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:544 M:283 W: Missing Blank Line separator, <220> field identifier
L:544 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:548 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:548 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:560 M:283 W: Missing Blank Line separator, <220> field identifier
L:560 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:568 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:568 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:578 M:283 W: Missing Blank Line separator, <220> field identifier
L:578 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:586 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:586 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11